

MODEL-BASED REGISTRATION TO CORRECT FOR MOTION BETWEEN ACQUISITIONS IN DIFFUSION MR IMAGING

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ABSTRACT

In diffusion tensor MRI, a number of diffusion-weighted images with different diffusion-weighting gradient directions are acquired during scanning. The tensor calculation assumes that each voxel corresponds to the same anatomical location in all the measurements. Movements and distortions violate this assumption and typically the images are realigned before model fitting. The traditional method uses a non-diffusion-weighted image as the reference for registration, but the differences between diffusion-weighted images and the non-diffusion weighted reference image can cause mismatching to occur during registration, even using metrics like the mutual information (MI) that accounts for non-linear contrast differences. We propose alternative model-based methods to improve motion correction and avoid the errors that the traditional method introduces. We demonstrate quantitative improvements using the new approaches on a full data with slight, but typical, movement during acquisition.

Index Terms— Diffusion, MRI, motion correction, model-based, registration

1. INTRODUCTION

Diffusion MRI (Magnetic Resonance Imaging) [1] has increased in popularity recently since the introduction of diffusion tensor (DT) MRI [2]. Diffusion MRI measures the local water diffusion properties in the material being imaged. In fibrous material, diffusion in directions perpendicular to the fibre is hindered by cell walls, so water diffuses more easily along axon bundles. Thus, diffusion MRI can be used to estimate fibre direction when combined with a suitable reconstruction method, such as DT-MRI [2].

Brain white matter fibres connect different regions of grey matter. By following fibre directions from point to point through the image, we can recover the trajectory of white matter fibres, which reveals the connectivity between the different regions of the brain.

Modern DT-MRI protocols acquire between 6 and about 100 diffusion-weighted (DW) images with different gradient directions. During such a long time, small head movements are not easy to avoid. In addition, DW-MRI uses a spin-echo

sequence with EPI readout, which induces further displacement and distortion in the images [3, 4]. However, the tensor calculation assumes that each voxel corresponds to the same anatomical location in all the measurements, so the images typically require prealignment.

The traditional method for DW-MRI registration uses a non-diffusion-weighted ($b = 0$) MR image as the reference for registration, since it does not suffer from eddy-current-induced distortion and has higher SNR than the DW images [5]. The scheme registers each DW image to the reference by a 3D rigid or affine transformation computed by maximizing a similarity measure such as cross-correlation or mutual information. The problem is that the differences between DW images and reference image cause mismatching. The differences can be highly localized confounding even information theoretic similarity measures like mutual information. To address these problems, this work proposes an alternative model-based registration technique to improve motion correction and correct the errors that the traditional method introduces. The method uses the DT model to predict separate reference images for each diffusion gradient.

2. BACKGROUND

2.1. Diffusion-tensor MRI

DT-MRI [2] fits the apparent diffusion tensor in each voxel to a number of measurements $A(\mathbf{q}_i), i = 1, \dots, N$, with different diffusion weighting. The model is

$$A(\mathbf{q}) = \exp(-t\mathbf{q}^T D \mathbf{q}), \quad (1)$$

where D is the diffusion tensor, t is the diffusion time and \mathbf{q} is a vector denoting the strength and direction of the diffusion weighting.

To fit the six free parameters of D requires a minimum of six measurements $A(\mathbf{q})$ with independent \mathbf{q} . To obtain less noisy DT-MR images, around 50 measurements are typically acquired. Most often, the linear least-squares algorithm is used to fit the tensor D to the log of the measurement via Eq. (1). Non-linear least squares fitting is slower but more appropriate for the noise in DW images. Also, various robust fitting procedures exist to avoid outliers from physiolog-

ical noise effects like cardiac pulsation. One example is the RESTORE algorithm [6], which we use later. The method detects outliers by thresholding the residual from the linear fit and then iteratively reweights measurements during non-linear fitting to reduce the influence of outliers.

Two useful scalar indices derived from D . Two of the most commonly used are the trace, $Tr(D)$, and the fractional anisotropy (FA). $Tr(D)$ is proportional to the mean squared displacement, and indicates the mobility of the water molecules. FA is the normalised standard deviation of the eigenvalues. High FA appear in areas in which the local fibres have consistent orientation.

2.2. DWI registration

The traditional method to align all the DW acquisitions in a DT-MRI protocol is to match each DWI to an unweighted ($b = 0$) image. A recent implementation of this idea is FM-RIB's Diffusion Toolbox, eddycorrect [7] which combines this strategy with the popular FLIRT tool [8]. Eddycorrect uses only shear to correct for eddy current distortions only. The dataset we use here has significant movement corruption, which is a rotation of the head. We adapt eddycorrect to use a full affine transformation for comparison with the new method we propose; we refer to this method henceforward as 'the traditional method'.

Two techniques in the literature are more similar to ours. Andersson and Skare [3] formulate a large optimization to correct misalignment and fit the DT model at the same time. However, the method is very computationally expensive. Moreover, the algorithm does not exclude outliers, which can cause the method often to converge on poor solutions. Buonaccorsi et al.[9] present a locally-controlled 3D translational registration process driven by tracer kinetic model of blood volume. Their technique involves fitting a parametric kinetic model to a time series of measurements in each voxel. They use a five-step iterative scheme in the registration process: **1.** Fit the model to the original measurements; **2.** Synthesize reference signal maps from the fitted model; **3.** Register translation only to match each original time point volume to its corresponding reference volume; **4.** Re-fit the model; **5.** Repeat steps 2 to 4 until a minimum is found in the model fit errors. This method copes well with features that appear and disappear between images, but, as with Andersson and Skare [3], does not account for outliers.

3. METHOD

Here, we adopt a similar approach to Buonaccorsi but adapted for DT-MRI. The basic framework contains three steps: **1.** Fit the model to the measurements; **2.** Synthesize reference data for each measurement from the fitted model; **3.** Register each measurement volume to the corresponding synthetic reference. This section outlines two versions of the method.

3.1. Fit the Model to All the Measurements - FMAM

The most direct model-based registration is a direct adaptation of Buonaccorsi's method [9] to DT-MRI. We call this the FMAM method. Since the method does not attempt to reject outliers, the model fitting procedure is influenced by measurements from misaligned images. **Step 1:** Fit the tensor to all scanner output measurement images, as described in §2.1. **Step 2:** Making synthetic images. From the fitted tensor D from step 1, we generate target image volumes for each measurement by synthesizing the measurement from Eq. (1). **Step 3:** Registration of the scanner output image data set. We register every DWI to the corresponding synthetic target image, with the same \mathbf{q} , using FLIRT [8] to perform 3D affine registration by optimizing mutual information.

Compared with the traditional method, FMAM has the advantage that it uses different reference images to register DW images with different gradient directions. The registration thus avoids mismatches that small local contrast differences can cause.

3.2. Fit the Model using RESTORE - FMR

Step 1 of FMAM fits the diffusion tensor D to the whole set of DW measurements. This means that all measurements, including any that are poorly aligned, contribute to the fitted D . The corrupted measurements therefore affect the reference image made from D in step 2.

We may expect better reference images, if we fit the tensor only to the uncorrupted subset of measurements. This section's alternative procedure (FMR) replaces step 1 above by fitting using the RESTORE method [6], which uses outlier rejection to ignore corrupted measurements. The RESTORE method was designed to improve DT fitting in the presence of motion artifacts caused, for example, by cardiac pulsation. Here, we use the technique slightly differently to eliminate misaligned measurements during reference construction.

3.3. Gradients Correction

The steps outlined the previous sections, including the traditional method mentioned in §2.2, do not account for the effect of rotation on the DWIs. Rotational head motion causes additional contrast changes because of the change in diffusion gradient direction with respect to the head. Figure 1 illustrates the effect. Having computed a correcting affine transformation for each acquisition, we update the effective diffusion-weighting gradient direction to account for the head rotation at imaging time. From the affine transformation T_i obtained from the registration, we use the standard polar decomposition [10] to extract the rotation R_i for each image:

$$R_i = (T_i T_i^T)^{-1/2} T_i, \quad (2)$$

and use it to correct each gradient direction $\mathbf{q}_i \rightarrow R_i(\mathbf{q}_i)$.

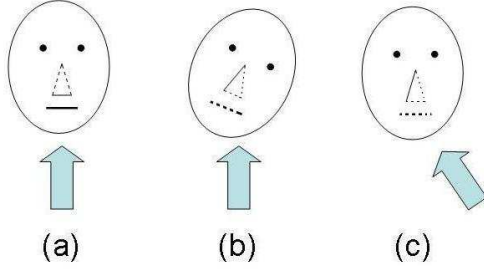


Fig. 1. Illustration of how rotation affects the effective gradient direction. The arrows indicate gradient directions. (a) Head without rotation. Suppose the mouth is a fibre. The signal is high because the gradient is perpendicular to the fibre. (b) Head with rotation. The signal is lower in the mouth fibre. (c) The unrotated head (after registration). The effective gradient direction for the corrected image is rotated.

We note here that we might iterate the whole procedure outlined at the start of this section, as in [9]. However, we find little improvement in practice after the first iteration so do not include that step here.

4. EXPERIMENTS AND RESULTS

We run the traditional method, and FMAM and FMR methods on a full dataset acquired on a Philips 3T Achieva scanner with small motion corruption, which has 64 measurements, with $128 \times 128 \times 32$ voxels for each measurement. The dataset has 60 diffusion weighted images with $b = 1200\text{s/mm}^2$. After aligning the data set, we also update diffusion gradients for the registered datasets from traditional, and FMAM and FMR methods, according to the transformations used in registrations.

As the original data set contains only small motion corruption, it is hard to tell the differences and improvement by visualising FA maps. Thus to assess the performance of different methods, we evaluate the variance of statistics derived from the diffusion tensor fitted to subsets of the 60 measurements in each voxel. The better aligned the 60 measurements, the more consistent statistics like FA, $\text{Tr}(\mathbf{D})$ and principle diffusion direction should be among different subsets of the 60 measurements. Specifically, we divide the 60 measurements into 4 groups of 15. We use the method in [11] to choose the four subsets so that each contains 15 measurements from well separated and evenly distributed directions. To evaluate the variance of the four principal directions $\mathbf{e}_1, \dots, \mathbf{e}_4$ in each voxel, we use the largest eigenvalue λ_1 of the dyadic tensor $\sum_{i=1}^4 \mathbf{e}_i \mathbf{e}_i^T$. When all four $|\mathbf{e}_i|$ are aligned, $\lambda_1 = 1$. As they become less aligned, λ_1 decreases to a minimum of zero when they are maximally separated.

Table 1 shows the average of λ_1 over four image regions after alignment using the various algorithms. One of the

regions is the whole of the skull-stripped brain. The other regions are shown in Figure 2. The first four rows of Table 1 compare three methods, traditional, FMAM and FMR, with no alignment. Those rows show mean λ_1 without the gradient-direction correction step in §3.3. The remaining rows compare mean λ_1 after gradient-direction correction.

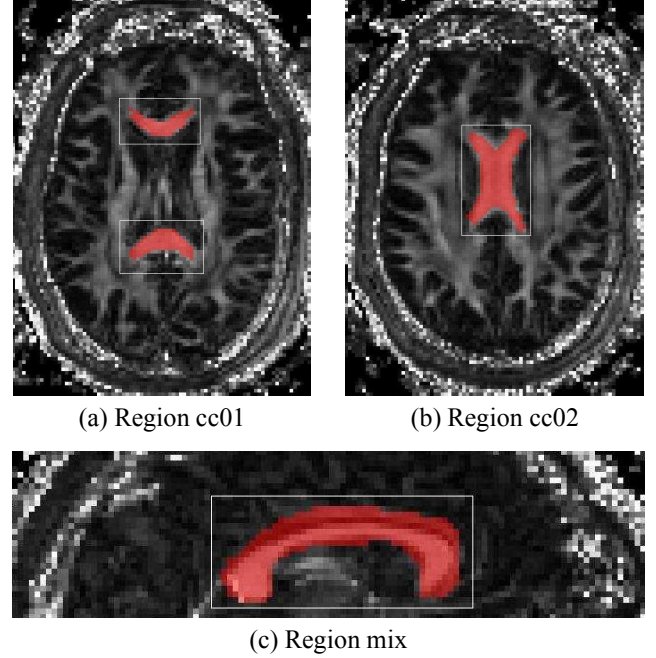


Fig. 2. Three specified regions (coloured in red) for comparing measurement's alignment.

	Brain	cc01	cc02	mix
Original data	0.8180	0.9961	0.9835	0.9065
Traditional	0.9206	0.9989	0.9959	0.9676
FMAM	0.9358	0.9989	0.9989	0.9811
FMR	0.9335	0.9989	0.9988	0.9804
Correction with Gradient Updated				
Traditional	0.9280	0.9988	0.9961	0.9623
FMAM	0.9364	0.9988	0.9987	0.9819
FMR	0.9350	0.9987	0.9987	0.9814

Table 1. Mean of λ_1 's of dyadic tensors in four region (the larger the better and 1 is perfect)

All three methods, with and without gradient updating, improve the alignment of the four sub-tensors. The FMAM and FMR methods give convincingly better performance than the traditional method. The extra step of correcting the diffusion gradients generally improves alignments slightly further.

The rotation component from Eq. (2) includes contribution from the shear caused by eddy-current distortion, which

	Brain	cc01	cc02	mix
Original data	0.2825	0.7067	0.6955	0.5248
Traditional	0.2164	0.6812	0.6201	0.4134
FMAM	0.2264	0.6939	0.6568	0.4715
FMR	0.2250	0.6912	0.6552	0.4740
Correction with Gradient Updated				
Traditional	0.2172	0.6803	0.6238	0.4089
FMAM	0.2266	0.6947	0.6574	0.4713
FMR	0.2258	0.6951	0.6597	0.4714

Table 2. Mean of FAs

does not affect the gradient orientation. We may see further improvement if we can separate the rotational corruption from motion and the eddy-current distortion and use only the former to correct gradient orientations. We note that in this example, FMR offers no advantage over FMAM. However, it introduces no significant disadvantage and, in cases with larger distortions or motion problems, it is often more robust solve advocate its use.

Table 2 shows the mean FA over the same regions used in Table 1. We observe an increase in FA using the new alignment procedures, which also suggests improved alignment reducing small partial-volume effects that artificially reduce FA.

5. DISCUSSION

For fitting the diffusion tensor, voxels in different diffusion-weighted images must correspond to the same anatomical location. Thus, all the measurement images need to be well aligned. The long scan time introduces patient movement. Moreover, EPI induces displacement and distortion in DW-MRI. The traditional correction schemes use the same reference image to register all the other diffusion-weighted images with different gradient directions. Although they correct the effects of both eddy-current-induced distortion and subject motion, local contrast differences still cause misregistration.

Here, we have proposed new model-based methods and tested them on a full-size diffusion MRI data set. The new methods are based on a three-step procedure to register DWI data sets. They use different reference images for DWIs with different gradient directions for registration, so the registrations take into account the contrast differences of measurements. FMAM fits the diffusion tensor D to the whole set of diffusion weighted measurements, and FMR fits the tensor only to a selected subset of measurement images.

Quantitative results show the FMAM and FMR provide significant improvement from the traditional alignment procedure, and orientation correction for the diffusion gradients upgrades the registration performance for all methods. Computation time for a typical dataset on a modern desktop is about 120mins, which is about the same as eddycorrect.

Acknowledgement: The authors would like to thank Geoff Parker and Karl Embleton, University of Manchester, for providing the brain data. EPSRC GR/T22858/05 and EP/E064590/1 fund DCA.

6. REFERENCES

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